GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 05:36:57 ; Search time 1812 Seconds
(without alignments)
9379.712 Million cell updates/sec

Title: US-09-695-451-1_COPY_727_1310
Perfect score: 584
Sequence: 1 tgccaggagaaacagaacac.....cacaagccacagagcctaga 584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 630880

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
1		24.8	4.2	28	6	A29671	A29671 Oligonucleo
2	c	23.8	4.1	29	6	A26411	A26411 oligonucleo
3		22.8	3.9	26	6	A29670	A29670 Oligonucleo
4		21	3.6	21	6	A19910	A19910 Synthetic 3
5	c	21	3.6	21	6	A19912	A19912 Synthetic 5
6	c	21	3.6	21	6	AR131319	AR131319 Sequence
7	c	21	3.6	21	6	AR134771	AR134771 Sequence
8	c	21	3.6	29	6	AX404882	AX404882 Sequence
9		20.8	3.6	24	6	A57512	A57512 Sequence 4
10		20.8	3.6	24	6	AR052978	AR052978 Sequence
11	c	20	3.4	30	6	A20243	A20243 Mutagenic o
12	c	20	3.4	30	6	I43796	I43796 Sequence 15
13		19.2	3.3	24	6	A57514	A57514 Sequence 6
14		19.2	3.3	24	6	AR052980	AR052980 Sequence
15		18.8	3.2	24	6	A57518	A57518 Sequence 10
16		18.8	3.2	24	6	AR052984	AR052984 Sequence
17	c	18.2	3.1	23	6	AX472525	AX472525 Sequence
18	c	18.2	3.1	25	6	AR074225	AR074225 Sequence
19	c	18.2	3.1	25	6	AR074226	AR074226 Sequence
20	c	18.2	3.1	25	6	AX032587	AX032587 Sequence
21	c	18.2	3.1	25	6	AX032588	AX032588 Sequence
22	c	18	3.1	18	6	AR096376	AR096376 Sequence
23	c	18	3.1	18	6	AR096377	AR096377 Sequence
24	c	18	3.1	18	6	AR096378	AR096378 Sequence
25	c	18	3.1	18	6	AR096379	AR096379 Sequence
26	c	18	3.1	18	6	AR096380	AR096380 Sequence
27	c	18	3.1	18	6	AR096381	AR096381 Sequence
28	c	18	3.1	18	6	AR096382	AR096382 Sequence
29	c	18	3.1	18	6	AR096383	AR096383 Sequence
30	c	18	3.1	18	6	AR096384	AR096384 Sequence
31	c	18	3.1	18	6	AR096385	AR096385 Sequence
32	c	18	3.1	18	6	AR096386	AR096386 Sequence
33	c	18	3.1	18	6	AR096387	AR096387 Sequence
34	c	18	3.1	18	6	AR096388	AR096388 Sequence
35	c	18	3.1	18	6	AR096389	AR096389 Sequence
36	c	18	3.1	18	6	AR096390	AR096390 Sequence
37	c	18	3.1	18	6	AR096391	AR096391 Sequence
38	c	18	3.1	18	6	AR096392	AR096392 Sequence
39	c	18	3.1	18	6	AR096393	AR096393 Sequence
40	c	18	3.1	18	6	AR096394	AR096394 Sequence
41	c	18	3.1	18	6	AR096395	AR096395 Sequence
42	c	18	3.1	18	6	AR096396	AR096396 Sequence
43	c	18	3.1	18	6	AR096397	AR096397 Sequence
44	c	18	3.1	18	6	AR096398	AR096398 Sequence
45	c	18	3.1	18	6	AR096399	AR096399 Sequence

ALIGNMENTS

RESULT 1
A29671
LOCUS A29671 28 bp DNA linear PAT 29-JUN-1995
DEFINITION Oligonucleotide no.2.
ACCESSION A29671
VERSION A29671.1 GI:1248974
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Wallach,D. and Brakebusch,C.
TITLE Multimers of the soluble forms of TNF receptors, their preparation and pharmaceutical compositions containing them
JOURNAL Patent: EP 0526905-A 2 10-FEB-1993;

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  Matches   26;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     248 AGTCCAAGCTCTACTCCATTGTTTGTGG 275
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Db       1 AGTCCAAGCTCTAGACCATTGTTTGTGG 28


RESULT 2
A26411/c
LOCUS       A26411                    29 bp    DNA     linear   PAT 25-APR-1995
DEFINITION  oligonucleotide  2 from patent EP0417563.
ACCESSION   A26411
VERSION     A26411.1  GI:904967
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 23 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT         5 a      7 c      9 g      8 t
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  Best Local Similarity   92.6%;  Pred. No. 9.8e+04;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     143 CTGAGGACTCAGGCACCACAGTGCTGT 169
           ||||||||||||||||||||| ||| |
Db      29 CTGAGGACTCAGGCACCACAGAGCTCT 3


RESULT 3
A29670
LOCUS       A29670                    26 bp    DNA     linear   PAT 29-JUN-1995
DEFINITION  Oligonucleotide no.1.
ACCESSION   A29670
VERSION     A29670.1  GI:1248973
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Wallach,D. and Brakebusch,C.
  TITLE     Multimers of the soluble forms of TNF receptors, their preparation
            and pharmaceutical compositions containing them
  JOURNAL   Patent: EP 0526905-A 1 10-FEB-1993;
            YEDA RESEARCH AND DEVELOPMENT CO. LTD
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT         6 a     10 c      7 g      3 t
ORIGIN

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  Best Local Similarity   92.3%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     531 CCCCAACCCCCTTCAGAAGTGGGAGG 556
           ||||||||||||  ||||||||||||
Db       1 CCCCAACCCCCTCTAGAAGTGGGAGG 26


RESULT 4
A19910
LOCUS       A19910                    21 bp    DNA     linear   PAT 04-OCT-1994
DEFINITION  Synthetic 3' TNF receptor fragment for construction of pSV-TBP.
ACCESSION   A19910
VERSION     A19910.1  GI:641224
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
            Aderka,D.
  TITLE     Expression of the recombinant tumor necrosis factor binding protein
            I (TBP-I)
  JOURNAL   Patent: EP 0433900-A 31 26-JUN-1991;
            YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT         6 a      6 c      4 g      5 t
ORIGIN

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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     112 TGCCTACCCCAGATTGAGAAT 132
           |||||||||||||||||||||
Db       1 TGCCTACCCCAGATTGAGAAT 21


RESULT 5
A19912/c
LOCUS       A19912                    21 bp    DNA     linear   PAT 04-OCT-1994
DEFINITION  Synthetic 5' TNF receptor fragment for construction of pSV-TBP.
ACCESSION   A19912
VERSION     A19912.1  GI:641226
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
            Aderka,D.
  TITLE     Expression of the recombinant tumor necrosis factor binding protein
            I (TBP-I)
  JOURNAL   Patent: EP 0433900-A 33 26-JUN-1991;
            YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     112 TGCCTACCCCAGATTGAGAAT 132
           |||||||||||||||||||||
Db      21 TGCCTACCCCAGATTGAGAAT 1
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RESULT 6
AR131319/c
LOCUS       AR131319                21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 19 from patent US 6193972.
ACCESSION   AR131319
VERSION     AR131319.1  GI:14120222
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Campbell,R.K., Jameson,B.A. and Chappel,S.C.
  TITLE     Hybrid heterodimeric protein hormone
  JOURNAL   Patent: US 6193972-A 19 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        2 a      5 c      7 g      7 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    142 ACTGAGGACTCAGGCACCACA 162
          |||||||||||||||||||||
Db     21 ACTGAGGACTCAGGCACCACA 1


RESULT 7
AR134771/c
LOCUS       AR134771                21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 19 from patent US 6194177.
ACCESSION   AR134771
VERSION     AR134771.1  GI:14123676
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Campbell,R.K., Jameson,B.A. and Chappel,S.C.
  TITLE     DNA encoding a hybrid heterodimeric protein
  JOURNAL   Patent: US 6194177-A 19 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        2 a      5 c      7 g      7 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    142 ACTGAGGACTCAGGCACCACA 162
          |||||||||||||||||||||
Db     21 ACTGAGGACTCAGGCACCACA 1


RESULT 8
AX404882/c
LOCUS       AX404882                29 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 15 from Patent WO0222833.
ACCESSION   AX404882
VERSION     AX404882.1  GI:21438114
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Pfizenmaier,K., Wuest,T., Moosmayer,D., Grell,M. and Scheurich,P.
  TITLE     Fusion protein from antibody cytokine-cytokine inhibitor
            (selectokine) for use as target-specific prodrug
  JOURNAL   Patent: WO 0222833-A 15 21-MAR-2002;
            Universitaet Stuttgart (DE) ; Pfizenmaier, Klaus (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer 6 fuer die Amplifikation eines
                     TNFR1-Fragments"
BASE COUNT        3 a      9 c     10 g      7 t
ORIGIN

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  Best Local Similarity   82.8%;  Pred. No. 5.8e+05;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy     13 CAGAACACCGTGTGCACCTGCCATGCAGG 41
          |||||||||||||||| |  |||||
Db     29 CAGAACACCGTGTGCACCGGATCCGCAGG 1


RESULT 9
A57512
LOCUS       A57512                  24 bp    DNA     linear   PAT 03-MAR-1998
DEFINITION  Sequence 4 from Patent WO9632483.
ACCESSION   A57512
VERSION     A57512.1  GI:3713370
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Masucci,M.G.
  TITLE     IMMUNE-EVADING PROTEINS
  JOURNAL   Patent: WO 9632483-A 4 17-OCT-1996;
            MASUCCI MARIA GRAZIA (SE)
COMMENT     Other publication AU 5284296 961030.
FEATURES             Location/Qualifiers
     source          1. .24
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Qy    399 TTCCACCTTCACCTCCAGCTCCAC 422
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Db      1 TTCCACCCGCACCTCCAGCTCCAC 24


RESULT 10
AR052978
LOCUS       AR052978                24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5833991.
ACCESSION   AR052978
VERSION     AR052978.1  GI:5977840
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Masucci,M.G.
  TITLE     Glycine-containing sequences conferring invisibility to the immune
            system
  JOURNAL   Patent: US 5833991-A 7 10-NOV-1998;
FEATURES             Location/Qualifiers
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Qy     399 TTCCACCTTCACCTCCAGCTCCAC 422
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Db       1 TTCCACCCGCACCTCCAGCTCCAC 24


RESULT 11
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LOCUS       A20243                   30 bp    DNA     linear   PAT 20-SEP-1995
DEFINITION  Mutagenic oligonucleotide 4D.
ACCESSION   A20243
VERSION     A20243.1  GI:1247885
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SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
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BASE COUNT        5 a      8 c     10 g      7 t
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RESULT 12
I43796/c
LOCUS       I43796                   30 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 15 from patent US 5633145.
ACCESSION   I43796
VERSION     I43796.1  GI:2468894
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE     TNF.alpha. receptor-derived binding protein
  JOURNAL   Patent: US 5633145-A 15 27-MAY-1997;
FEATURES             Location/Qualifiers
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 CAGAACACCGTGTGCACCTG 32
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Db      30 CAGAACACCGTGTGCACCTG 11


RESULT 13
A57514
LOCUS       A57514                   24 bp    DNA     linear   PAT 03-MAR-1998
DEFINITION  Sequence 6 from Patent WO9632483.
ACCESSION   A57514
VERSION     A57514.1  GI:3713372
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Masucci,M.G.
  TITLE     IMMUNE-EVADING PROTEINS
  JOURNAL   Patent: WO 9632483-A 6 17-OCT-1996;
            MASUCCI MARIA GRAZIA (SE)
COMMENT     Other publication AU 5284296 961030.
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Db        1 TTCCACCCGCACCTCCAGCTCCTC 24


RESULT 14
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DEFINITION  Sequence 10 from patent US 5833991.
ACCESSION   AR052980
VERSION     AR052980.1  GI:5977842
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Masucci,M.G.
  TITLE     Glycine-containing sequences conferring invisibility to the immune
            system
  JOURNAL   Patent: US 5833991-A 10 10-NOV-1998;
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DEFINITION  Sequence 10 from Patent WO9632483.
ACCESSION   A57518
VERSION     A57518.1  GI:3713376
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SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Masucci,M.G.
  TITLE     IMMUNE-EVADING PROTEINS
  JOURNAL   Patent: WO 9632483-A 10 17-OCT-1996;
            MASUCCI MARIA GRAZIA (SE)
COMMENT     Other publication AU 5284296 961030.
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Job time : 1814 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:22:44 ; Search time 221 Seconds
(without alignments)
5950.982 Million cell updates/sec

Title: US-09-695-451-1_COPY_727_1310
Perfect score: 584
Sequence: 1 tgccaggagaaacagaacac.....cacaagccacagagcctaga 584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 1875172

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
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13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	25	4.3	25	21	AAA95191	Reverse primer use
c	2	23.8	4.1	29	20	AAZ09169	Human 55kDa tumour
c	3	23.8	4.1	29	22	AAH48858	Human 55 kD TNFBP
c	4	21	3.6	21	18	AAT94017	Primer for TPO/hCG
c	5	21	3.6	29	24	ABA99921	Human TNFR1 PCR pr
	6	20.8	3.6	24	19	AAV55815	Multimerisation of
	7	19.2	3.3	24	19	AAV55817	Multimerisation of
c	8	19.2	3.3	27	22	AAF24737	PCR primer used to
	9	19.2	3.3	30	20	AAX27663	DNA encoding a HRG
	10	19.2	3.3	30	24	ABL51730	HRGP related oligo
	11	19.2	3.3	30	24	ABL51739	Hydroxyproline-ric
	12	18.8	3.2	24	19	AAV55821	Multimerisation of
c	13	18.8	3.2	30	17	AAT17807	Glycosaminoglycan-
c	14	18.4	3.2	30	24	ABL51740	Hydroxyproline-ric
c	15	18.2	3.1	23	24	ABK97993	Cell-TRAP method a
c	16	18.2	3.1	25	15	AAQ61892	HSV replication in
c	17	18.2	3.1	25	15	AAQ61893	HSV replication in
c	18	18.2	3.1	25	16	AAQ97978	Peptide nucleic ac
c	19	18	3.1	18	18	AAT87450	p55 extracellular
c	20	18	3.1	18	19	AAV03624	3' primer for p55
c	21	18	3.1	18	20	AAX81714	Primer used to con
c	22	18	3.1	18	21	AAZ48521	Human TNFR1 mRNA i
c	23	18	3.1	18	21	AAZ48522	Human TNFR1 mRNA i
c	24	18	3.1	18	21	AAZ48523	Human TNFR1 mRNA i
c	25	18	3.1	18	21	AAZ48524	Human TNFR1 mRNA i
c	26	18	3.1	18	21	AAZ48525	Human TNFR1 mRNA i
c	27	18	3.1	18	21	AAZ48526	Human TNFR1 mRNA i
c	28	18	3.1	18	21	AAZ48527	Human TNFR1 mRNA i
c	29	18	3.1	18	21	AAZ48528	Human TNFR1 mRNA i
c	30	18	3.1	18	21	AAZ48529	Human TNFR1 mRNA i
c	31	18	3.1	18	21	AAZ48530	Human TNFR1 mRNA i
c	32	18	3.1	18	21	AAZ48531	Human TNFR1 mRNA i
c	33	18	3.1	18	21	AAZ48532	Human TNFR1 mRNA i
c	34	18	3.1	18	21	AAZ48533	Human TNFR1 mRNA i
c	35	18	3.1	18	21	AAZ48534	Human TNFR1 mRNA i
c	36	18	3.1	18	21	AAZ48535	Human TNFR1 mRNA i
c	37	18	3.1	18	21	AAZ48536	Human TNFR1 mRNA i
c	38	18	3.1	18	21	AAZ48537	Human TNFR1 mRNA i
c	39	18	3.1	18	21	AAZ48538	Human TNFR1 mRNA i
c	40	18	3.1	18	21	AAZ48539	Human TNFR1 mRNA i
c	41	18	3.1	18	21	AAZ48540	Human TNFR1 mRNA i
c	42	18	3.1	18	21	AAZ48541	Human TNFR1 mRNA i
c	43	18	3.1	18	21	AAZ48542	Human TNFR1 mRNA i
c	44	18	3.1	18	21	AAZ48543	Human TNFR1 mRNA i
c	45	18	3.1	18	21	AAZ48544	Human TNFR1 mRNA i

ALIGNMENTS

RESULT 1
AAA95191/c
ID AAA95191 standard; DNA; 25 BP.
XX
AC AAA95191;
XX
DT 12-JAN-2001 (first entry)
XX
DE Reverse primer used to amplify exon 6 of TNFR1 gene.
XX
KW TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW tumour; cancer; apoptosis; bacterial infection; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200050436-A1.
XX
PD 31-AUG-2000.
XX
PF 23-FEB-2000; 2000WO-US04606.
XX
PR 23-FEB-1999; 99US-0121314.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (NAND/) NANDABALAN K.
PA (SCHU/) SCHULZ V P.
PA (STEP/) STEPHENS J C.
PA (CHEW/) CHEW A.
XX
PI Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX
DR WPI; 2000-543909/49.

XX
PT Polynucleotides comprising polymorphic variants of a reference sequence
PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
PT biological function of TNFR1 and identifying drugs targeting the
PT protein for treating disorders -
XX
PS Example 1; Page 31; 79pp; English.
XX
CC The present invention relates to polymorphic variants of the tumour
CC necrosis factor receptor 1 (TNFR1) gene. The sequence of the gene is
CC given in AAA95102, AAA95103 and AAA95104. The polymorphisms were
CC identified by amplifying and sequencing regions of the gene. Twelve
CC polymorphic loci were discovered. Of these twelve polymorphisms, four can
CC cause a change in the TNFR1 protein. The present sequence is a primer
CC used to amplify part of the TNFR1 gene. The TNFR1 polymorphisms may be
CC useful for studying the biological function of TNFR1 as well as for
CC identifying drugs targeting the protein for treatment of disorders
CC related to its abnormal expression or function such as tumours,
CC apoptosis related disorders and bacterial infection.
XX
SQ Sequence 25 BP; 5 A; 8 C; 4 G; 8 T; 0 other;

Query Match 4.3%; Score 25; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 GAATGTTAAGGGCACTGAGGACTCA 153
||||||||||||||||||||||||||
Db 25 GAATGTTAAGGGCACTGAGGACTCA 1

RESULT 2
AAZ09169/c
ID AAZ09169 standard; DNA; 29 BP.
XX
AC AAZ09169;
XX
DT 18-OCT-1999 (first entry)
XX
DE Human 55kDa tumour necrosis factor binding protein PCR primer 2.
XX
KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW autoimmune glomerulonephritis; cerebral malaria; immune response;
KW antagonist; diagnosis; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP939121-A2.
XX
PD 01-SEP-1999.
XX
PF 31-AUG-1990; 90EP-0116707.
XX
PR 20-APR-1990; 90CH-0001347.
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX
DR WPI; 1999-480840/41.
XX
PT New insoluble proteins, and fragments, that bind to tumor necrosis
PT factor, used to treat e.g. septic shock or cerebral malaria
XX
PS Example 11; Page 16; 25pp; German.
XX
CC This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence represents
CC a PCR primer used in the amplification of the TNF binding protein of the
CC invention.
XX
SQ Sequence 29 BP; 5 A; 7 C; 9 G; 8 T; 0 other;

Query Match 4.1%; Score 23.8; DB 20; Length 29;
Best Local Similarity 92.6%; Pred. No. 2.6e+03;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 143 CTGAGGACTCAGGCACCACAGTGCTGT 169
|||||||||||||||||||| ||| |
Db 29 CTGAGGACTCAGGCACCACAGAGCTCT 3

RESULT 3
AAH48858/c
ID AAH48858 standard; DNA; 29 BP.
XX
AC AAH48858;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human 55 kD TNFBP extracellular fragment PCR primer 2.
XX
KW TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN EP1132471-A2.
XX
PD 12-SEP-2001.
XX
PF 31-AUG-1990; 2001EP-0108117.
XX
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
PR 20-APR-1990; 90CH-0001347.
PR 31-AUG-1990; 90EP-0116707.
PR 31-AUG-1990; 99EP-0100703.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX
DR WPI; 2001-559312/63.
XX
PT New homogeneous, insoluble proteins that bind tumor necrosis factor
PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
XX
PS Example 11; Page 16; 26pp; German.
XX
CC This invention describes novel insoluble proteins (I), also their
CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC invention have antiinflammatory, immunosuppressive, antibacterial,
CC antiprotozoal activity. (I), and related recombinant proteins, are used
CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC sepsis; development of autoimmune glomerulonephritis and cerebral
CC malaria. Also (I), or antibodies specific for them, are used for
CC diagnostic determination of TNF in body fluids, for affinity purification
CC of TNF and for identifying (ant)agonists of TNF. This sequence represents
CC a PCR primer used in the amplification of the human 55 kD TNFBP described

```
CC   in the method of the invention.
XX
SQ   Sequence 29 BP; 5 A; 7 C; 9 G; 8 T; 0 other;

  Query Match           4.1%;  Score 23.8;  DB 22;  Length 29;
  Best Local Similarity  92.6%;  Pred. No. 2.6e+03;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     143 CTGAGGACTCAGGCACCACAGTGCTGT 169
           ||||||||||||||||||||| ||| |
Db      29 CTGAGGACTCAGGCACCACAGAGCTCT 3


RESULT 4
AAT94017/c
ID   AAT94017 standard; DNA; 21 BP.
XX
AC   AAT94017;
XX
DT   19-MAR-1998  (first entry)
XX
DE   Primer for TPO/hCG fusion gene.
XX
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   hCG; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9730161-A1.
XX
PD   21-AUG-1997.
XX
PF   20-FEB-1997;   97WO-US02315.
XX
PR   20-FEB-1996;   96US-0011936.
XX
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI   Campbell RK,  Chappel SC,  Jameson BA;
XX
DR   WPI; 1997-425036/39.
XX
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
XX
PS   Example; Page 16; 60pp; English.
XX
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin (hCG) fusion
CC   protein encoded by the fusion gene amplified by the present
CC   sequence, significantly increases the biological activity of the
CC   hormone component, reducing the requirement for hormone itself and
CC   the number of injections needed.
XX
SQ   Sequence 21 BP; 2 A; 5 C; 7 G; 7 T; 0 other;

  Query Match           3.6%;  Score 21;  DB 18;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+04;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     142 ACTGAGGACTCAGGCACCACA 162
           |||||||||||||||||||||
Db      21 ACTGAGGACTCAGGCACCACA 1


RESULT 5
ABA99921/c
ID   ABA99921 standard; DNA; 29 BP.
XX
AC   ABA99921;
XX
DT   05-JUL-2002  (first entry)
XX
DE   Human TNFR1 PCR primer SEQ ID 15.
XX
KW   Prodrug; TNF; tumour necrosis factor; selectokine; chimeric; W24; W33;
KW   cytostatic; immunomodulatory; antiangiogenic; apoptosis inducer;
KW   gene therapy; scFv antibody OS4; fibroblast activation protein; tenascin;
KW   solid tumour; angiogenesis; treatment; infection; metabolic disease;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200222833-A1.
XX
PD   21-MAR-2002.
XX
PF   17-SEP-2001; 2001WO-EP10730.
XX
PR   15-SEP-2000; 2000DE-1045592.
XX
PA   (UYST-) UNIV STUTTGART.
PA   (PFIZ/) PFIZENMAIER K.
XX
PI   Pfizenmaier K,  Wuest T,  Moosmayer D,  Grell M,  Scheurich P;
XX
DR   WPI; 2002-362351/39.
XX
PT   New polypeptide prodrug, useful e.g. for treating tumors, contains
PT   targeting region, active agent and attached inhibitor that is
PT   proteolytically cleaved in target cells -
XX
PS   Example 6; Page 47; 52pp; German.
XX
CC   This invention describes a novel polypeptide (I) comprising, in the N
CC   to C direction, a region (R1) that recognises selectively a specific
CC   macromolecule on a cell surface and/or a component of the extracellular
CC   matrix, peptide linker, a region (R2) with biological activity for a
CC   specific target molecule, a region (R3) that has a processing site and a
CC   region (R4) that inhibits the activity of R2, by intramolecular bonding
CC   and/or interaction. The products of the invention have cytostatic,
CC   immunomodulatory and antiangiogenic activity, induce apoptosis and can be
CC   used for gene therapy. Kym-1 cells (20000) were incubated with the
CC   prodrug W24, containing, essentially, the single-chain Fv antibody OS4,
CC   specific for human fibroblast activation protein, trimerization linker,
CC   mutant form of the tumour necrosis factor (TNF) precursor protein, a
CC   region with a proteolytic cleavage site, and human TNF receptor-1
CC   fragment, and with trypsin (activator) for 5 minutes. After 16 hours,
CC   cell viability was determined by MTT staining. Activated W24 had LD50
CC   about 0.5 ng/ml, comparable with that for wild-type TNF and 4000 times
CC   higher than for uncleaved W24. (I), also nucleic acids encoding them and
CC   related vectors, are useful particularly for treating solid tumours
CC   and/or pathological angiogenesis, also generally for treating infections
CC   and metabolic diseases. (I) are prodrug forms of R2 that have
CC   unacceptable toxicity when administered systemically (specifically tumour
CC   necrosis factor) and allow these compounds to be administered safely with
CC   retention of, or even increase in, therapeutic activity. R2 is released
CC   only in target tissue, resulting in a high local concentration, and
CC   activity is potentiated by co-activation of receptors. This sequence
CC   represents a PCR primer for the amplification of the human TNFR1 fragment
CC   used in the construction of the TNF-selectokine W24 and W33
CC   prodrugs described in the disclosure of the invention.
XX
SQ   Sequence 29 BP; 3 A; 9 C; 10 G; 7 T; 0 other;

  Query Match           3.6%;  Score 21;  DB 24;  Length 29;
  Best Local Similarity  82.8%;  Pred. No. 1.7e+04;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy      13 CAGAACACCGTGTGCACCTGCCATGCAGG 41
           ||||||||||||||||| |    |||||
Db      29 CAGAACACCGTGTGCACCGGATCCGCAGG 1


RESULT 6
AAV55815
ID   AAV55815 standard; DNA; 24 BP.
XX
AC   AAV55815;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Multimerisation of minimal motifs using primer ZGS2.
XX
KW   Fusion protein; stabilising polypeptide; proteolytic degradation;
KW   resistance; half-life; autoimmune disease; inflammation; nitro drug;
KW   IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
KW   nitroreductase protein; enzyme therapy; prodrug therapy; protease;
KW   cancer; pathological condition; minimal motif; PCR primer; ss.
XX
OS   Synthetic.
OS   Epstein-barr virus.
XX
PN   WO9822577-A1.
XX
PD   28-MAY-1998.
XX
PF   17-NOV-1997;   97WO-IB01508.
XX
PR   25-JUN-1997;   97US-0048945.
PR   15-NOV-1996;   96US-0030986.
XX
PA   (MASU/) MASUCCI M G.
XX
PI   Masucci MG;
XX
DR   WPI; 1998-312463/27.
XX
PT   New fusion proteins resistant to proteolytic degradation -
PT   comprising a core protein with a stabilising polypeptide comprising
PT   a peptide sequence containing glycine repeats
XX
PS   Disclosure; Page 72; 120pp; English.
XX
CC   Sequences shown in AAV55812 to AAV55827 represent primers used in the
CC   course of the invention for the multimerisation of minimal motifs. The
CC   invention provides a method for increasing the resistance of a core
CC   protein to proteolytic degradation that comprises linking or inserting
CC   onto or into the core protein a stabilising polypeptide of formula
CC   [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly
CC   residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr
CC   and n can be anything between 1-66. X, Y and Z need not be identical
CC   from n repeat to n repeat. Alternatively a nucleic acid encoding a
CC   stabilising polypeptide can be linked onto or inserted into a nucleic
CC   acid encoding a core protein. The fusion proteins of the invention are
CC   more resistant to degradation by proteases and, thus, have a longer
CC   half-life than the unfused core protein. The products can be used for
CC   treating autoimmune diseases, cancer and inflammation. In particular, the
CC   core protein may be an IkappaB regulator protein for the treatment of
CC   inflammatory bowel disease, or a nitroreductase protein which can
CC   activate nitro drugs in enzyme/prodrug therapy to treat cancer or other
CC   pathological conditions. The fusion proteins can also be used in
CC   diagnostic methods such as in vivo imaging.
XX
SQ   Sequence 24 BP; 4 A; 14 C; 2 G; 4 T; 0 other;

  Query Match             3.6%;  Score 20.8;  DB 19;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 1.8e+04;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     399 TTCCACCTTCACCTCCAGCTCCAC 422
           |||||||  ||||||||||||||||
Db       1 TTCCACCCGCACCTCCAGCTCCAC 24


RESULT 7
AAV55817
ID   AAV55817 standard; DNA; 24 BP.
XX
AC   AAV55817;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Multimerisation of minimal motifs using primer ZGR2.
XX
KW   Fusion protein; stabilising polypeptide; proteolytic degradation;
KW   resistance; half-life; autoimmune disease; inflammation; nitro drug;
KW   IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
KW   nitroreductase protein; enzyme therapy; prodrug therapy; protease;
KW   cancer; pathological condition; minimal motif; PCR primer; ss.
XX
OS   Synthetic.
OS   Epstein-barr virus.
XX
PN   WO9822577-A1.
XX
PD   28-MAY-1998.
XX
PF   17-NOV-1997;   97WO-IB01508.
XX
PR   25-JUN-1997;   97US-0048945.
PR   15-NOV-1996;   96US-0030986.
XX
PA   (MASU/) MASUCCI M G.
XX
PI   Masucci MG;
XX
DR   WPI; 1998-312463/27.
XX
PT   New fusion proteins resistant to proteolytic degradation -
PT   comprising a core protein with a stabilising polypeptide comprising
PT   a peptide sequence containing glycine repeats
XX
PS   Disclosure; Page 72; 120pp; English.
XX
CC   Sequences shown in AAV55812 to AAV55827 represent primers used in the
CC   course of the invention for the multimerisation of minimal motifs. The
CC   invention provides a method for increasing the resistance of a core
CC   protein to proteolytic degradation that comprises linking or inserting
CC   onto or into the core protein a stabilising polypeptide of formula
CC   [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly
CC   residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr
CC   and n can be anything between 1-66. X, Y and Z need not be identical
CC   from n repeat to n repeat. Alternatively a nucleic acid encoding a
CC   stabilising polypeptide can be linked onto or inserted into a nucleic
CC   acid encoding a core protein. The fusion proteins of the invention are
CC   more resistant to degradation by proteases and, thus, have a longer
CC   half-life than the unfused core protein. The products can be used for
CC   treating autoimmune diseases, cancer and inflammation. In particular, the
CC   core protein may be an IkappaB regulator protein for the treatment of
CC   inflammatory bowel disease, or a nitroreductase protein which can
CC   activate nitro drugs in enzyme/prodrug therapy to treat cancer or other
CC   pathological conditions. The fusion proteins can also be used in
CC   diagnostic methods such as in vivo imaging.
XX
SQ   Sequence 24 BP; 3 A; 14 C; 2 G; 5 T; 0 other;

  Query Match             3.3%;  Score 19.2;  DB 19;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 5.1e+04;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     399 TTCCACCTTCACCTCCAGCTCCAC 422
           |||||||  |||||||||||||  |
Db       1 TTCCACCCGCACCTCCAGCTCCTC 24
```

```
RESULT 8
AAF24737/c
ID   AAF24737 standard; DNA; 27 BP.
XX
AC   AAF24737;
XX
DT   20-APR-2001  (first entry)
XX
DE   PCR primer used to amplify DNA encoding CDB-Tma peptide.
XX
KW   Protein production; food processing; protein antibiotic; feed enzyme;
KW   CBD-Tma; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200077174-A1.
XX
PD   21-DEC-2000.
XX
PF   07-JUN-2000; 2000WO-IL00330.
XX
PR   10-JUN-1999;   99US-0329234.
XX
PA   (CBDT-) CBD TECHNOLOGIES LTD.
PA   (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI   Shani Z,  Shoseyov O;
XX
DR   WPI; 2001-112219/12.
XX
PT   Expressing and isolating recombinant protein in a plant, useful for
PT   producing large quantities of recombinant proteins, by expressing a
PT   fusion protein including a cellulose binding peptide fused to a
PT   recombinant protein
XX
PS   Example; Page 48; 87pp; English.
XX
CC   The specification describes a method for expressing and isolating
CC   a recombinant protein in a plant. The method comprising expressing a
CC   fusion protein including the recombinant protein and a cellulose
CC   binding peptide fused to it, where the fusion protein is
CC   compartmentalised and sequestered within plant cells, plant derived
CC   tissue or cultured plant cells. The method is useful for obtaining large
CC   quantities of the recombinant proteins and protein products in a simple
CC   and cost-effective manner. Recombinant proteins may be used commercially,
CC   such as in the food processing industry, e.g. glucoamylases and glucose
CC   isomerases are used for converting starch to high fructose corn syrup,
CC   proteinases for the hydrolysis of high molecular weight proteins and in
CC   manufacturing leather or alcoholic beverages, pectinesterases for
CC   pectin hydrolysis in food industry, lipases for cleaving ester linkage
CC   in triglycerides, and for effluent treatment. The recombinant proteins
CC   may further be used to produce protein antibiotics, which can be used
CC   in healing processes, and to produce animal feed enzymes. PCR primers
CC   AAF24736-37 were used to amplify DNA encoding a CBD-Tma peptide. The
CC   amplified fragment was used to produce the fusion proteins of the
CC   invention.
XX
SQ   Sequence 27 BP; 7 A; 4 C; 12 G; 4 T; 0 other;

  Query Match             3.3%;  Score 19.2;  DB 22;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 5.3e+04;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    520 TCCGACCCCATCCCCAACCCCCTT 543
          |||||||||||||||||| |  ||
Db     26 TCCGACCCCATCCCCAACGCGTTT 3


RESULT 9
AAX27663
ID   AAX27663 standard; DNA; 30 BP.
XX
AC   AAX27663;
XX
DT   01-JUN-1999  (first entry)
XX
DE   DNA encoding a HRGP motif.
XX
KW   Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP;
KW   repetitive proline-rich protein; RPRP; arabino-galactan protein; AGP;
KW   glycopeptide; ss.
XX
OS   Acacia sp.
XX
PN   WO9903978-A1.
XX
PD   28-JAN-1999.
XX
PF   21-JUL-1998;   98WO-US15083.
XX
PR   20-JUL-1998;   98US-0897556.
PR   21-JUL-1997;   97US-0897556.
XX
PA   (UYOH-) UNIV OHIO.
XX
PI   Kielszewski MJ;
XX
DR   WPI; 1999-132225/11.
XX
PT   Novel synthetic gene designed from repetitive peptide sequences - of
PT   hydroxyproline-rich glycoprotein
XX
PS   Claim 1; Page 5; 72pp; English.
XX
CC   The invention relates to novel synthetic genes for plant gums. A new
CC   approach is described to the production of hydroxyproline-rich
CC   glycoproteins (HRGPs), repetitive proline-rich proteins (RPRPs) and
CC   arabino-galactan proteins (AGPs). Synthetic genes comprising a nucleic
CC   acid encoding the peptide (AAY01267) can be engineered for the
CC   production of repetitive glycopeptide modules in cells. The invention
CC   provided a new approach to the problem of producing plant gums that is
CC   not dependent on environmental factors and greatly simplifies the
CC   production of a variety of naturally occurring gums as well as designer
CC   gums. Note: The present nucleotide sequence is indicated as a peptide
CC   sequence in the claims.
XX
SQ   Sequence 30 BP; 6 A; 19 C; 0 G; 5 T; 0 other;

  Query Match             3.3%;  Score 19.2;  DB 20;  Length 30;
  Best Local Similarity   87.5%;  Pred. No. 5.5e+04;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    401 CCACCTTCACCTCCAGCTCCACCT 424
          |||||||||||||||| | ||| ||
Db      4 CCACCTTCACCTCCACCCCCATCT 27


RESULT 10
ABL51730
ID   ABL51730 standard; DNA; 30 BP.
XX
AC   ABL51730;
XX
DT   09-JUL-2002  (first entry)
XX
DE   HRGP related oligonucleotide SEQ ID NO:10.
XX
KW   Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
KW   HRGP; repetitive proline-rich protein; RPRP; arabinogalactan protein;
KW   AGP; plant gum; PCR primer; linker; ss.
XX
OS   Acacia senegal.
OS   Synthetic.
XX
PN   WO200178503-A2.
```

```
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US12336.
XX
PR   12-APR-2000; 2000US-0547693.
XX
PA   (UYOH-) UNIV OHIO.
XX
PI   Kieliszewski MJ;
XX
DR   WPI; 2002-041307/05.
XX
PT   Nucleic acids and proteins useful for producing hydroxy-proline rich
PT   glycoproteins in plants -
XX
PS   Disclosure; Page 4-5; 326pp; English.
XX
CC   The present invention describes synthetic genes encoding plant gums and
CC   other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic
CC   acids that encode them. The nucleic acids, proteins and methods from the
CC   present invention may be used to produce HRGPs, repetitive proline-rich
CC   proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via
CC   recombinant methodologies. Also described is the expression of synthetic
CC   genes designed from repetitive peptide sequences, such as glycoproteins
CC   (including the peptide sequences of gum arabic glycoprotein (GAGP)).
CC   ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used
CC   in the exemplification of the present invention.
XX
SQ   Sequence 30 BP; 6 A; 19 C; 0 G; 5 T; 0 other;

  Query Match              3.3%;  Score 19.2;  DB 24;  Length 30;
  Best Local Similarity   87.5%;  Pred. No. 5.5e+04;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     401 CCACCTTCACCTCCAGCTCCACCT 424
           |||||||||||||||| | ||| ||
Db       4 CCACCTTCACCTCCACCCCCATCT 27


RESULT 11
ABL51739
ID   ABL51739 standard; DNA; 30 BP.
XX
AC   ABL51739;
XX
DT   09-JUL-2002  (first entry)
XX
DE   Hydroxyproline-rich glycoprotein (HRGP) related linker SEQ ID NO:38.
XX
KW   Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
KW   HRGP; repetitive proline-rich protein; RPRP; arabinogalactan protein;
KW   AGP; plant gum; PCR primer; linker; ss.
XX
OS   Acacia senegal.
OS   Synthetic.
XX
PN   WO200178503-A2.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US12336.
XX
PR   12-APR-2000; 2000US-0547693.
XX
PA   (UYOH-) UNIV OHIO.
XX
PI   Kieliszewski MJ;
XX
DR   WPI; 2002-041307/05.
XX
PT   Nucleic acids and proteins useful for producing hydroxy-proline rich
PT   glycoproteins in plants -
XX
PS   Example 2; Page 53; 326pp; English.
XX
CC   The present invention describes synthetic genes encoding plant gums and
CC   other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic
CC   acids that encode them. The nucleic acids, proteins and methods from the
CC   present invention may be used to produce HRGPs, repetitive proline-rich
CC   proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via
CC   recombinant methodologies. Also described is the expression of synthetic
CC   genes designed from repetitive peptide sequences, such as glycoproteins
CC   (including the peptide sequences of gum arabic glycoprotein (GAGP)).
CC   ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used
CC   in the exemplification of the present invention.
XX
SQ   Sequence 30 BP; 6 A; 19 C; 0 G; 5 T; 0 other;

  Query Match              3.3%;  Score 19.2;  DB 24;  Length 30;
  Best Local Similarity   87.5%;  Pred. No. 5.5e+04;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     401 CCACCTTCACCTCCAGCTCCACCT 424
           |||||||||||||||| | ||| ||
Db       4 CCACCTTCACCTCCACCCCCATCT 27


RESULT 12
AAV55821
ID   AAV55821 standard; DNA; 24 BP.
XX
AC   AAV55821;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Multimerisation of minimal motifs using primer ZGY2.
XX
KW   Fusion protein; stabilising polypeptide; proteolytic degradation;
KW   resistance; half-life; autoimmune disease; inflammation; nitro drug;
KW   IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
KW   nitroreductase protein; enzyme therapy; prodrug therapy; protease;
KW   cancer; pathological condition; minimal motif; PCR primer; ss.
XX
OS   Synthetic.
OS   Epstein-barr virus.
XX
PN   WO9822577-A1.
XX
PD   28-MAY-1998.
XX
PF   17-NOV-1997;   97WO-IB01508.
XX
PR   25-JUN-1997;   97US-0048945.
PR   15-NOV-1996;   96US-0030986.
XX
PA   (MASU/) MASUCCI M G.
XX
PI   Masucci MG;
XX
DR   WPI; 1998-312463/27.
XX
PT   New fusion proteins resistant to proteolytic degradation -
PT   comprising a core protein with a stabilising polypeptide comprising
PT   a peptide sequence containing glycine repeats
XX
PS   Disclosure; Page 72; 120pp; English.
XX
CC   Sequences shown in AAV55812 to AAV55827 represent primers used in the
CC   course of the invention for the multimerisation of minimal motifs. The
CC   invention provides a method for increasing the resistance of a core
CC   protein to proteolytic degradation that comprises linking or inserting
CC   onto or into the core protein a stabilising polypeptide of formula
CC   [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly
CC   residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr
CC   and n can be anything between 1-66. X, Y and Z need not be identical
```

CC from n repeat to n repeat. Alternatively a nucleic acid encoding a
CC stabilising polypeptide can be linked onto or inserted into a nucleic
CC acid encoding a core protein. The fusion proteins of the invention are
CC more resistant to degradation by proteases and, thus, have a longer
CC half-life than the unfused core protein. The products can be used for
CC treating autoimmune diseases, cancer and inflammation. In particular, the
CC core protein may be an IkappaB regulator protein for the treatment of
CC inflammatory bowel disease, or a nitroreductase protein which can
CC activate nitro drugs in enzyme/prodrug therapy to treat cancer or other
CC pathological conditions. The fusion proteins can also be used in
CC diagnostic methods such as in vivo imaging.
XX
SQ Sequence 24 BP; 5 A; 13 C; 2 G; 4 T; 0 other;

Query Match 3.2%; Score 18.8; DB 19; Length 24;
Best Local Similarity 90.9%; Pred. No. 6.6e+04;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 400 TCCACCTTCACCTCCAGCTCCA 421
||||||| ||||||||||||||
Db 2 TCCACCCGCACCTCCAGCTCCA 23

RESULT 13
AAT17807/c
ID AAT17807 standard; DNA; 30 BP.
XX
AC AAT17807;
XX
DT 30-OCT-1996 (first entry)
XX
DE Glycosaminoglycan-degrading enzyme inhibitor LG5PS.
XX
KW Glycosaminoglycan-degrading enzyme; GDE; inhibitor; endoglycosidase;
KW heparanase; heparitinase; mammalian; bacterial; platelet; macrophage;
KW neutrophil; leukocyte; endothelial cell; smooth muscle cell; carcinoma;
KW tumour cell; activation; proliferation; migration; cancer; inflammation;
KW autoimmune disorder; infection; pathogenic organism; atherosclerosis;
KW cardiovascular disease; vascular hyperplasia; restenosis; therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..30
FT /*tag= a
FT /note= "phosphorothioate, or phosphorodithioate backbone"
XX
PN WO9608559-A1.
XX
PD 21-MAR-1996.
XX
PF 13-SEP-1995; 95WO-AU00600.
XX
PR 14-AUG-1995; 95AU-0004769.
PR 16-SEP-1994; 94AU-0008226.
PR 16-SEP-1994; 94AU-0008227.
XX
PA (CARD-) CARDIAC CRC NOMINEES PTY LTD.
XX
PI Graham L, Underwood PA;
XX
DR WPI; 1996-179936/18.
XX
PT Oligo:nucleotide(s) having sulphur substns. between nucleoside(s)
PT for inhibiting glycosaminoglycan-degrading enzymes, for treating,
PT e.g. cancer, inflammation, infection or autoimmune disorders.
XX
PS Claim 6; Page 33; 73pp; English.
XX
CC AAT17805-T17808, and AAT17810-T17813 represent
CC glycosaminoglycan-degrading enzyme (GDE) inhibitors. The GDEs which
CC these sequences inhibit are endoglycosidases (which cleave
CC glycosaminoglycan chains at internal sites), preferably heparanases (also
CC known as heparitinases) of mammalian or bacterial origin. These
CC sequences can be used for inhibiting GDEs associated with platelets,
CC macrophages, neutrophils, leukocytes, endothelial cells, smooth muscle
CC cells, carcinoma and tumour cells, and bacteria. They can also be used
CC to inhibit smooth muscle cell activation, proliferation or migration.
CC The sequences can be used to treat cancer, inflammation, autoimmune
CC disorders, infection caused by pathogenic organisms, and cardiovascular
CC disease, such as vascular hyperplasia, restenosis and atherosclerosis.
CC These inhibitors can also be used as biochemical reagents for studying
CC GDE activities and mechanisms of enzyme activity.
XX
SQ Sequence 30 BP; 0 A; 5 C; 20 G; 5 T; 0 other;

Query Match 3.2%; Score 18.8; DB 17; Length 30;
Best Local Similarity 76.7%; Pred. No. 7.2e+04;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 511 GCCCTCGCCTCCGACCCCATCCCCAACCCC 540
| || || | |||||||| |||| |||||
Db 30 GACCCCGACCCCGACCCCGACCCCGACCCC 1

RESULT 14
ABL51740/c
ID ABL51740 standard; DNA; 30 BP.
XX
AC ABL51740;
XX
DT 09-JUL-2002 (first entry)
XX
DE Hydroxyproline-rich glycoprotein (HRGP) related linker SEQ ID NO:39.
XX
KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
KW HRGP; repetitive proline-rich protein; RPRP; arabinogalactan protein;
KW AGP; plant gum; PCR primer; linker; ss.
XX
OS Acacia senegal.
OS Synthetic.
XX
PN WO200178503-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US12336.
XX
PR 12-APR-2000; 2000US-0547693.
XX
PA (UYOH-) UNIV OHIO.
XX
PI Kieliszewski MJ;
XX
DR WPI; 2002-041307/05.
XX
PT Nucleic acids and proteins useful for producing hydroxy-proline rich
PT glycoproteins in plants -
XX
PS Example 2; Page 53; 326pp; English.
XX
CC The present invention describes synthetic genes encoding plant gums and
CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic
CC acids that encode them. The nucleic acids, proteins and methods from the
CC present invention may be used to produce HRGPs, repetitive proline-rich
CC proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via
CC recombinant methodologies. Also described is the expression of synthetic
CC genes designed from repetitive peptide sequences, such as glycoproteins
CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).
CC ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 30 BP; 5 A; 0 C; 19 G; 6 T; 0 other;

Query Match 3.2%; Score 18.4; DB 24; Length 30;
Best Local Similarity 78.6%; Pred. No. 9.4e+04;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy    402 CACCTTCACCTCCAGCTCCACCTATACC 429
          ||||| |||| ||| |||||||   |||
Db     29 CACCTCCACCCCCATCTCCACCACCACC 2
```

RESULT 58
ABK97993/c
ID ABK97993 standard; DNA; 23 BP.
XX
AC ABK97993;
XX
DT 07-OCT-2002 (first entry)
XX
DE Cell-TRAP method associated GATA mut oligonucleotide.
XX
KW Transcription factor; transcription factor-responsive element;
KW ds; TFRE; transcription activation; Cell-TRAP.
XX
OS Synthetic.
XX
PN WO200252039-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-CA01861.
XX
PR 27-DEC-2000; 2000CA-2327581.
XX
PA (GENE-) GENEKA BIOTECHNOLOGY INC.
XX
PI Blais Y, Rousseau P, Leblanc B, Camato RN;
XX
DR WPI; 2002-575388/61.
XX
PT A Cell-TRAP method, useful for producing or validating therapeutic
PT compounds, by employing a recombinant cell-based library that carry
PT constructs driven by a minimal promoter and a transcription
PT factor-responsive element -
XX
PS Disclosure; Page 24; 44pp; English.
XX
CC This invention relates to a cell-TRAP method for selecting and producing
CC a therapeutic compound which is presumed selective for, one or a
CC restricted set of given transcriptional pathways and cell types by
CC employing a recombinant cell-based library that carries a construct
CC comprising a reporter gene driven by a minimal promoter and a
CC transcription factor-responsive element (TFRE). The invention also
CC comprises a method for validating a putative compound as a selective
CC therapeutic compound towards a transcription factor response element.
CC The method of the invention is useful for determining the
CC transcriptional activation pathways used by any compound that is
CC biologically active in a cell. This method allows a global view of gene
CC transcription activation in response to diverse stimuli in multiple
CC environments and is a significant improvement over case-by-case
CC approaches, which would be limited to certain aspects of gene
CC activation. It permits to save on clinical trials by screening properly
CC the compounds that would have a lesser probability of providing
CC undesirable, even severe side effects. The present sequence
CC represents a double stranded oligonucleotide probe recognised by a
CC specific transcription factor which is used in the method of the
CC invention.
XX
SQ Sequence 23 BP; 2 A; 9 C; 8 G; 4 T; 0 other;

Query Match 3.1%; Score 18.2; DB 24; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+04;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    457 CCCCGCAGAGAGGTGGCACCACC 479
          | ||||||||||||||||||  ||
Db     23 CGCCGCAGAGAGGTGGCACTGCC 1
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Search completed: May 21, 2003, 06:35:23
Job time : 223 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 06:16:20 ; Search time 75 Seconds
(without alignments)
2387.990 Million cell updates/sec

Title: US-09-695-451-1_COPY_727_1310
Perfect score: 584
Sequence: 1 tgccaggagaaacagaacac.....cacaagccacagagcctaga 584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 452144

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	21	3.6	21	4	US-08-804-166-19	Sequence 19, Appl
c	2	21	3.6	21	4	US-08-910-991-19	Sequence 19, Appl
	3	20.8	3.6	24	2	US-08-529-190B-7	Sequence 7, Appli
c	4	20	3.4	30	1	US-08-050-319B-15	Sequence 15, Appl
c	5	20	3.4	30	2	US-08-465-982-15	Sequence 15, Appl
	6	19.2	3.3	24	2	US-08-529-190B-10	Sequence 10, Appl
	7	18.8	3.2	24	2	US-08-529-190B-16	Sequence 16, Appl
c	8	18.2	3.1	25	2	US-08-403-888A-33	Sequence 33, Appl
c	9	18.2	3.1	25	2	US-08-403-888A-34	Sequence 34, Appl
c	10	18	3.1	18	1	US-08-192-102-15	Sequence 15, Appl
c	11	18	3.1	18	1	US-08-324-799-15	Sequence 15, Appl
c	12	18	3.1	18	2	US-08-192-861A-15	Sequence 15, Appl
c	13	18	3.1	18	3	US-09-106-038A-47	Sequence 47, Appl
c	14	18	3.1	18	3	US-09-106-038A-48	Sequence 48, Appl
c	15	18	3.1	18	3	US-09-106-038A-49	Sequence 49, Appl
c	16	18	3.1	18	3	US-09-106-038A-50	Sequence 50, Appl
c	17	18	3.1	18	3	US-09-106-038A-51	Sequence 51, Appl
c	18	18	3.1	18	3	US-09-106-038A-52	Sequence 52, Appl
c	19	18	3.1	18	3	US-09-106-038A-53	Sequence 53, Appl
c	20	18	3.1	18	3	US-09-106-038A-54	Sequence 54, Appl
c	21	18	3.1	18	3	US-09-106-038A-55	Sequence 55, Appl
c	22	18	3.1	18	3	US-09-106-038A-56	Sequence 56, Appl
c	23	18	3.1	18	3	US-09-106-038A-57	Sequence 57, Appl
c	24	18	3.1	18	3	US-09-106-038A-58	Sequence 58, Appl
c	25	18	3.1	18	3	US-09-106-038A-59	Sequence 59, Appl
c	26	18	3.1	18	3	US-09-106-038A-60	Sequence 60, Appl
c	27	18	3.1	18	3	US-09-106-038A-61	Sequence 61, Appl
c	28	18	3.1	18	3	US-09-106-038A-62	Sequence 62, Appl
c	29	18	3.1	18	3	US-09-106-038A-63	Sequence 63, Appl
c	30	18	3.1	18	3	US-09-106-038A-64	Sequence 64, Appl
c	31	18	3.1	18	3	US-09-106-038A-65	Sequence 65, Appl
c	32	18	3.1	18	3	US-09-106-038A-66	Sequence 66, Appl
c	33	18	3.1	18	3	US-09-106-038A-67	Sequence 67, Appl
c	34	18	3.1	18	3	US-09-106-038A-68	Sequence 68, Appl
c	35	18	3.1	18	3	US-09-106-038A-69	Sequence 69, Appl
c	36	18	3.1	18	3	US-09-106-038A-70	Sequence 70, Appl
c	37	18	3.1	18	4	US-09-133-119-15	Sequence 15, Appl
c	38	18	3.1	18	4	US-08-192-093A-15	Sequence 15, Appl
	39	18	3.1	24	4	US-08-697-610-11	Sequence 11, Appl
	40	18	3.1	24	4	US-08-349-357-11	Sequence 11, Appl
	41	17.8	3.0	23	1	US-08-474-542A-150	Sequence 150, App
	42	17.8	3.0	23	1	US-08-474-542A-151	Sequence 151, App
	43	17.8	3.0	23	1	US-08-457-648-150	Sequence 150, App
	44	17.8	3.0	23	1	US-08-457-648-151	Sequence 151, App
	45	17.8	3.0	24	2	US-08-529-190B-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-08-804-166-19/c
; Sequence 19, Application US/08804166
; Patent No. 6193972
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/011,936
;      FILING DATE:  20 February 1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-804-166-19

  Query Match             3.6%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy    142 ACTGAGGACTCAGGCACCACA 162
          |||||||||||||||||||||
Db     21 ACTGAGGACTCAGGCACCACA 1


RESULT 2
US-08-910-991-19/c
; Sequence 19, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
;   APPLICANT:  Campbell, Robert K.
;   APPLICANT:  Jameson, Bradford A.
;   APPLICANT:  Chappel, Scott C.
;   TITLE OF INVENTION:  HYBRID PROTEINS
;   NUMBER OF SEQUENCES:  22
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BROWDY AND NEIMARK
;     STREET:  419 Seventh Street N.W., Ste. 300
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  USA
;     ZIP:  22207
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/910,991
;     FILING DATE:
;     CLASSIFICATION:  530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/804,166
;     FILING DATE:  20 February 1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  60/011,936
;     FILING DATE:  20 February 1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  YUN, Allen C.
;     REGISTRATION NUMBER:  37,971
;     REFERENCE/DOCKET NUMBER:  CAMPBELL-2B
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202) 628-5197
;     TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  19:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  21 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
US-08-910-991-19

  Query Match             3.6%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    142 ACTGAGGACTCAGGCACCACA 162
          |||||||||||||||||||||
Db     21 ACTGAGGACTCAGGCACCACA 1


RESULT 3
US-08-529-190B-7
; Sequence 7, Application US/08529190B
; Patent No. 5833991
;  GENERAL INFORMATION:
;   APPLICANT:  Masucci, Maria G.
;   TITLE OF INVENTION:  GLYCINE-CONTAINING SEQUENCES
;   TITLE OF INVENTION:  CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
;   NUMBER OF SEQUENCES:  76
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Banner & Witcoff, Ltd.
;     STREET:  One Financial Center
;     CITY:  Boston
;     STATE:  MA
;     COUNTRY:  USA
;     ZIP:  02111
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  Wordperfect 6.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/529,190B
;     FILING DATE:  15-SEP-1995
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  SE9501324-9
;     FILING DATE:  10-APR-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US08/522,595
;     FILING DATE:  01-SEP-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Williams, Ph.D., Kathleen A
;     REGISTRATION NUMBER:  34,380
;     REFERENCE/DOCKET NUMBER:  3255/53015
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-345-9100
;     TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  24 bases
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  other nucleic acid
US-08-529-190B-7

  Query Match             3.6%;  Score 20.8;  DB 2;  Length 24;
  Best Local Similarity  91.7%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    399 TTCCACCTTCACCTCCAGCTCCAC 422
          |||||||  ||||||||||||||||
Db      1 TTCCACCCGCACCTCCAGCTCCAC 24


RESULT 4
US-08-050-319B-15/c
; Sequence 15, Application US/08050319B
; Patent No. 5633145
;  GENERAL INFORMATION:
;   APPLICANT:  M.Feldmann, P.W. Gray,
;   APPLICANT:  M.J.C. Turner, F.M Brennan
;   TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;   TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;   NUMBER OF SEQUENCES:  57
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Reed & Robbins
;     STREET:  635 Bryant Street
;     CITY:  Palo Alto
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94301
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/050,319B
;     FILING DATE:  10-May-1993
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Robbins, Roberta L.
```

```
;       REGISTRATION NUMBER:  33,208
;       REFERENCE/DOCKET NUMBER:  5150-0030
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 617-8999
;       TELEFAX:  (415) 327-3231
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  30 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-050,319B-15

  Query Match             3.4%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 CAGAACACCGTGTGCACCTG 32
           ||||||||||||||||||||
Db      30 CAGAACACCGTGTGCACCTG 11


RESULT 5
US-08-465-982-15/c
; Sequence 15, Application US/08465982
; Patent No. 5863786
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,982
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319
;      FILING DATE:  10-May-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-465-982-15

  Query Match             3.4%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 CAGAACACCGTGTGCACCTG 32
           ||||||||||||||||||||
Db      30 CAGAACACCGTGTGCACCTG 11


RESULT 6
US-08-529-190B-10
; Sequence 10, Application US/08529190B
; Patent No. 5833991
;  GENERAL INFORMATION:
;    APPLICANT:  Masucci, Maria G.
;    TITLE OF INVENTION:  GLYCINE-CONTAINING SEQUENCES
;    TITLE OF INVENTION:  CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  Wordperfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/529,190B
;      FILING DATE:  15-SEP-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE9501324-9
;      FILING DATE:  10-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US08/522,595
;      FILING DATE:  01-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen A
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3255/53015
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-529-190B-10

  Query Match             3.3%;  Score 19.2;  DB 2;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 4.7e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     399 TTCCACCTTCACCTCCAGCTCCAC 422
           |||||||  |||||||||||||| |
Db       1 TTCCACCCGCACCTCCAGCTCCTC 24


RESULT 7
US-08-529-190B-16
; Sequence 16, Application US/08529190B
; Patent No. 5833991
;  GENERAL INFORMATION:
;    APPLICANT:  Masucci, Maria G.
;    TITLE OF INVENTION:  GLYCINE-CONTAINING SEQUENCES
;    TITLE OF INVENTION:  CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center
;      CITY:  Boston
;      STATE:  MA
```

```
;       COUNTRY:  USA
;       ZIP:  02111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  Wordperfect 6.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/529,190B
;       FILING DATE:  15-SEP-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  SE9501324-9
;       FILING DATE:  10-APR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US08/522,595
;       FILING DATE:  01-SEP-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Williams, Ph.D., Kathleen A
;       REGISTRATION NUMBER:  34,380
;       REFERENCE/DOCKET NUMBER:  3255/53015
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-345-9100
;       TELEFAX:  617-345-9111
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
US-08-529-190B-16

  Query Match             3.2%;  Score 18.8;  DB 2;  Length 24;
  Best Local Similarity   90.9%;  Pred. No. 6.2e+03;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     400 TCCACCTTCACCTCCAGCTCCA 421
           ||||||  ||||||||||||||||
Db       2 TCCACCCGCACCTCCAGCTCCA 23


RESULT 8
US-08-403-888A-33/c
; Sequence 33, Application US/08403888A
; Patent No. 5952490
;  GENERAL INFORMATION:
;    APPLICANT:  Hanecak et al.
;    TITLE OF INVENTION:  Oligonucleotides Having A Conserved G4 Core
;    TITLE OF INVENTION:  Sequence
;    NUMBER OF SEQUENCES:  146
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,888A
;      FILING DATE:  12-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/954,185
;      FILING DATE:  29-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul K. Legaard
;      REGISTRATION NUMBER:  38,534
;      REFERENCE/DOCKET NUMBER:  ISIS-1229
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-403-888A-33

  Query Match             3.1%;  Score 18.2;  DB 2;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     518 CCTCCGACCCCATCCCCAACCCC 540
           || || ||||||||||||||||||
Db      25 CCCCCAACCCCAACCCCAACCCC 3


RESULT 9
US-08-403-888A-34/c
; Sequence 34, Application US/08403888A
; Patent No. 5952490
;  GENERAL INFORMATION:
;    APPLICANT:  Hanecak et al.
;    TITLE OF INVENTION:  Oligonucleotides Having A Conserved G4 Core
;    TITLE OF INVENTION:  Sequence
;    NUMBER OF SEQUENCES:  146
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,888A
;      FILING DATE:  12-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/954,185
;      FILING DATE:  29-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul K. Legaard
;      REGISTRATION NUMBER:  38,534
;      REFERENCE/DOCKET NUMBER:  ISIS-1229
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-403-888A-34

  Query Match             3.1%;  Score 18.2;  DB 2;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     518 CCTCCGACCCCATCCCCAACCCC 540
           || || ||||||||||||||||||
Db      25 CCCCCAACCCCAACCCCAACCCC 3
```

```
RESULT 10
US-08-192-102-15/c
; Sequence 15, Application US/08192102
; Patent No. 5656272
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,102
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,093
;      FILING DATE:  04-FEB-1994
;      APPLICATION NUMBER:  US 08/013,413
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/010,406
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,852
;      FILING DATE:  11-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,606
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/670,827
;      FILING DATE:  18-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  NYU93-01M3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-192-102-15

  Query Match             3.1%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     109 TTGTGCCTACCCCAGATT 126
           ||||||||||||||||||
Db      18 TTGTGCCTACCCCAGATT 1


RESULT 11
```

```
US-08-324-799-15/c
; Sequence 15, Application US/08324799
; Patent No. 5698195
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES AND PEPTIDES
;    TITLE OF INVENTION:  OF HUMAN TUMOR NECROSIS FACTOR
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,799
;      FILING DATE:  18-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,093
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,102
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,861
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/013,413
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/010,406
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,852
;      FILING DATE:  11-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,606
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/670,827
;      FILING DATE:  18-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  NYU93-01M4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-324-799-15

  Query Match             3.1%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     109 TTGTGCCTACCCCAGATT 126
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              ||||||||||||||||||
Db      18 TTGTGCCTACCCCAGATT 1


RESULT 12
US-08-192-861A-15/c
; Sequence 15, Application US/08192861A
; Patent No. 5919452
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  METHODS OF TREATING TNF'-MEDIATED DISEASE USING
;    TITLE OF INVENTION:  CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,861A
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/013,413
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/010,406
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,852
;      FILING DATE:  11-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,606
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/670,827
;      FILING DATE:  18-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  NYU93-01M2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (781) 861-6240
;      TELEFAX:  (781) 861-9540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-192-861A-15

  Query Match             3.1%;  Score 18;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     109 TTGTGCCTACCCCAGATT 126
           ||||||||||||||||||
Db      18 TTGTGCCTACCCCAGATT 1


RESULT 13
US-09-106-038A-47/c
; Sequence 47, Application US/09106038A
; Patent No. 6007995
;  GENERAL INFORMATION:
;    APPLICANT:  Brenda F. Baker and Lex M. Cowsert
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF TNFR1
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Isis Pharmaceuticals, Inc.
;      STREET:  2292 Faraday Avenue
;      CITY:  Carlsbad
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  Microsoft Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,038A
;      FILING DATE:  June 26, 1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Laurel Spear Bernstein
;      REGISTRATION NUMBER:  37,280
;      REFERENCE/DOCKET NUMBER:  RTS-0004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (760) 931-9200
;      TELEFAX:  (760) 603-3820
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-106-038A-47

  Query Match             3.1%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 GGAGAAACAGAACACCGT 23
           ||||||||||||||||||
Db      18 GGAGAAACAGAACACCGT 1


RESULT 14
US-09-106-038A-48/c
; Sequence 48, Application US/09106038A
; Patent No. 6007995
;  GENERAL INFORMATION:
;    APPLICANT:  Brenda F. Baker and Lex M. Cowsert
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF TNFR1
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Isis Pharmaceuticals, Inc.
;      STREET:  2292 Faraday Avenue
;      CITY:  Carlsbad
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  Microsoft Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,038A
;      FILING DATE:  June 26, 1998
```

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;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Laurel Spear Bernstein
;      REGISTRATION NUMBER:  37,280
;      REFERENCE/DOCKET NUMBER:  RTS-0004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (760) 931-9200
;      TELEFAX:  (760) 603-3820
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-106-038A-48

  Query Match             3.1%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      60 CGAGTGTGTCTCCTGTAG 77
           ||||||||||||||||||
Db      18 CGAGTGTGTCTCCTGTAG 1


RESULT 15
US-09-106-038A-49/c
; Sequence 49, Application US/09106038A
; Patent No. 6007995
;  GENERAL INFORMATION:
;    APPLICANT:  Brenda F. Baker and Lex M. Cowsert
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF TNFR1
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Isis Pharmaceuticals, Inc.
;      STREET:  2292 Faraday Avenue
;      CITY:  Carlsbad
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  Microsoft Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,038A
;      FILING DATE:  June 26, 1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Laurel Spear Bernstein
;      REGISTRATION NUMBER:  37,280
;      REFERENCE/DOCKET NUMBER:  RTS-0004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (760) 931-9200
;      TELEFAX:  (760) 603-3820
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-106-038A-49

  Query Match             3.1%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      70 TCCTGTAGTAACTGTAAG 87
           ||||||||||||||||||
Db      18 TCCTGTAGTAACTGTAAG 1
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Search completed: May 21, 2003, 07:31:30
Job time : 77 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 06:31:36 ; Search time 128 Seconds
(without alignments)
6024.609 Million cell updates/sec

Title: US-09-695-451-1_COPY_727_1310
Perfect score: 584
Sequence: 1 tgccaggagaaacagaacac.....cacaagccacagagcctaga 584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 375196

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	5.1	30	9	US-09-898-234-9	Sequence 9, Appli
2	30	5.1	30	9	US-09-792-356-9	Sequence 9, Appli
3	30	5.1	30	10	US-09-899-422-9	Sequence 9, Appli
c 4	21	3.6	21	10	US-09-756-186-19	Sequence 19, Appl
5	18.8	3.2	30	10	US-09-828-034-7	Sequence 7, Appli
c 6	18.2	3.1	23	9	US-10-113-877-128	Sequence 128, App
c 7	18	3.1	18	9	US-10-043-432-15	Sequence 15, Appl
c 8	18	3.1	18	10	US-09-756-301A-15	Sequence 15, Appl
c 9	18	3.1	18	10	US-09-927-703-15	Sequence 15, Appl
c 10	18	3.1	18	10	US-09-766-535A-15	Sequence 15, Appl
c 11	18	3.1	18	10	US-09-756-161A-15	Sequence 15, Appl
c 12	18	3.1	18	12	US-10-010-229-15	Sequence 15, Appl
c 13	18	3.1	18	12	US-10-043-450-15	Sequence 15, Appl
c 14	18	3.1	18	12	US-10-044-534-15	Sequence 15, Appl
15	18	3.1	24	10	US-09-757-041-11	Sequence 11, Appl
c 16	18	3.1	30	10	US-09-810-502-25	Sequence 25, Appl
c 17	17.4	3.0	30	9	US-10-085-906-221	Sequence 221, App
18	16.8	2.9	21	9	US-09-949-427-355	Sequence 355, App
19	16.2	2.8	29	9	US-09-746-783-203	Sequence 203, App
20	15.8	2.7	27	9	US-09-949-427-56	Sequence 56, Appl
c 21	15.8	2.7	27	10	US-09-735-363A-3	Sequence 3, Appli
c 22	15.8	2.7	27	10	US-09-735-363A-68	Sequence 68, Appl
c 23	15.8	2.7	28	9	US-10-023-066A-15	Sequence 15, Appl
24	15.8	2.7	29	10	US-09-756-283A-4	Sequence 4, Appli
c 25	15.6	2.7	25	9	US-10-215-112-1996	Sequence 1996, Ap
c 26	15.6	2.7	25	9	US-10-215-112-2122	Sequence 2122, Ap
c 27	15.6	2.7	25	10	US-09-866-108-13915	Sequence 13915, A
c 28	15.6	2.7	25	10	US-09-866-108-13916	Sequence 13916, A
c 29	15.6	2.7	25	10	US-09-866-108-13917	Sequence 13917, A
c 30	15.6	2.7	25	10	US-09-866-108-13918	Sequence 13918, A
c 31	15.6	2.7	25	10	US-09-441-522-29	Sequence 29, Appl
c 32	15.6	2.7	29	10	US-09-745-763-216	Sequence 216, App
33	15.6	2.7	30	9	US-09-886-156-4	Sequence 4, Appli
c 34	15.6	2.7	30	9	US-09-911-176B-4	Sequence 4, Appli
35	15.6	2.7	30	9	US-10-073-353-7	Sequence 7, Appli
36	15.6	2.7	30	9	US-09-886-150-4	Sequence 4, Appli
37	15.6	2.7	30	9	US-09-886-149-4	Sequence 4, Appli
38	15.6	2.7	30	9	US-09-886-159-4	Sequence 4, Appli
c 39	15.6	2.7	30	9	US-10-180-762-4	Sequence 4, Appli
40	15.6	2.7	30	9	US-10-057-467-12	Sequence 12, Appl
c 41	15.6	2.7	30	9	US-10-241-258-4	Sequence 4, Appli
42	15.6	2.7	30	10	US-09-828-313-87	Sequence 87, Appl
43	15.6	2.7	30	10	US-09-828-310-33	Sequence 33, Appl
44	15.6	2.7	30	10	US-09-828-447-33	Sequence 33, Appl
c 45	15.6	2.7	30	10	US-09-441-522-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-898-234-9
; Sequence 9, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(30)
US-09-898-234-9

Query Match 5.1%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GTTAAGGGCACTGAGGACTCAGGCACCACA 162
||||||||||||||||||||||||||||||
Db 1 GTTAAGGGCACTGAGGACTCAGGCACCACA 30

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RESULT 2
US-09-792-356-9
; Sequence 9, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-G
;  CURRENT APPLICATION NUMBER: US/09/792,356
;  CURRENT FILING DATE:  2001-08-17
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(30)
US-09-792-356-9

  Query Match             5.1%;  Score 30;  DB 9;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    133 GTTAAGGGCACTGAGGACTCAGGCACCACA 162
          ||||||||||||||||||||||||||||||
Db      1 GTTAAGGGCACTGAGGACTCAGGCACCACA 30


RESULT 3
US-09-899-422-9
; Sequence 9, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(30)
US-09-899-422-9

  Query Match             5.1%;  Score 30;  DB 10;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    133 GTTAAGGGCACTGAGGACTCAGGCACCACA 162
          ||||||||||||||||||||||||||||||
Db      1 GTTAAGGGCACTGAGGACTCAGGCACCACA 30


RESULT 4
US-09-756-186-19/c
; Sequence 19, Application US/09756186
; Patent No. US20010014333A1
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/756,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL-2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-756-186-19

  Query Match             3.6%;  Score 21;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    142 ACTGAGGACTCAGGCACCACA 162
          |||||||||||||||||||||
Db     21 ACTGAGGACTCAGGCACCACA 1


RESULT 5
```

```
US-09-828-034-7
; Sequence 7, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
;  APPLICANT: Zhong, Weidong
;  APPLICANT: Zhong, Zhi
;  APPLICANT: Ferrari, Eric
;  TITLE OF INVENTION: HCV REPLICASE COMPLEXES
;  FILE REFERENCE: IN01165
;  CURRENT APPLICATION NUMBER: US/09/828,034
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: U.S. 60/195,852
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;    LENGTH: 30
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-7

  Query Match             3.2%;  Score 18.8;  DB 10;  Length 30;
  Best Local Similarity  76.7%;  Pred. No. 1.6e+04;
  Matches   23;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     511 GCCCTCGCCTCCGACCCCATCCCCAACCCC 540
           |||| |||| ||| ||||  ||||  ||||
Db       1 GCCCCCGCCCCCGCCCCCGCCCCCGCCCCC 30


RESULT 6
US-10-113-877-128/c
; Sequence 128, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
;    LENGTH: 23
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: oligonucleotide
US-10-113-877-128

  Query Match             3.1%;  Score 18.2;  DB 9;  Length 23;
  Best Local Similarity  87.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     457 CCCCGCAGAGAGGTGGCACCACC 479
           | ||||||||||||||||  ||
Db      23 CGCCGCAGAGAGGTGGCACTGCC 1


RESULT 7
US-10-043-432-15/c
; Sequence 15, Application US/10043432
; Publication No. US20030054004A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/10/043,432
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: PCR oligonucleotides
US-10-043-432-15

  Query Match             3.1%;  Score 18;  DB 9;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     109 TTGTGCCTACCCCAGATT 126
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Db      18 TTGTGCCTACCCCAGATT 1


RESULT 8
US-09-756-301A-15/c
; Sequence 15, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-008
;  CURRENT APPLICATION NUMBER: US/09/756,301A
;  CURRENT FILING DATE:  2001-01-08
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;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S.07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR oligonucleotides
US-09-756-301A-15

  Query Match             3.1%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    109 TTGTGCCTACCCCAGATT 126
          ||||||||||||||||||
Db     18 TTGTGCCTACCCCAGATT 1


RESULT 9
US-09-927-703-15/c
; Sequence 15, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/09/927,703
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR oligonucleotides
US-09-927-703-15

  Query Match             3.1%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    109 TTGTGCCTACCCCAGATT 126
          ||||||||||||||||||
Db     18 TTGTGCCTACCCCAGATT 1


RESULT 10
US-09-766-535A-15/c
; Sequence 15, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-010
;  CURRENT APPLICATION NUMBER: US/09/766,535A
;  CURRENT FILING DATE:  2001-01-18
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR oligonucleotides
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US-09-766-535A-15

Query Match 3.1%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 TTGTGCCTACCCCAGATT 126
||||||||||||||||||
Db 18 TTGTGCCTACCCCAGATT 1

RESULT 11
US-09-756-161A-15/c
; Sequence 15, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S.07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR oligonucleotides
US-09-756-161A-15

Query Match 3.1%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 TTGTGCCTACCCCAGATT 126
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Db 18 TTGTGCCTACCCCAGATT 1

RESULT 12
US-10-010-229-15/c
; Sequence 15, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR oligonucleotides
US-10-010-229-15

Query Match 3.1%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 TTGTGCCTACCCCAGATT 126
||||||||||||||||||
Db 18 TTGTGCCTACCCCAGATT 1

RESULT 13
US-10-043-450-15/c
; Sequence 15, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827

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;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR oligonucleotides
US-10-043-450-15

  Query Match             3.1%;  Score 18;  DB 12;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     109 TTGTGCCTACCCCAGATT 126
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Db      18 TTGTGCCTACCCCAGATT 1


RESULT 14
US-10-044-534-15/c
; Sequence 15, Application US/10044534
; Patent No. US20020146419A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/10/044,534
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR oligonucleotides
US-10-044-534-15

  Query Match             3.1%;  Score 18;  DB 12;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     109 TTGTGCCTACCCCAGATT 126
           ||||||||||||||||||
Db      18 TTGTGCCTACCCCAGATT 1


RESULT 15
US-09-757-041-11
; Sequence 11, Application US/09757041
; Patent No. US20020009726A1
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Sato, Takaaki
;    TITLE OF INVENTION:  CD40 Associated Proteins
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/757,041
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/349,357
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1203
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-757-041-11

  Query Match             3.1%;  Score 18;  DB 10;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       7 CGCTACCAACGGTGGAAG 24


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Job time : 129 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 06:14:45 ; Search time 1439 Seconds
(without alignments)
6572.734 Million cell updates/sec

Title: US-09-695-451-1_COPY_727_1310
Perfect score: 584
Sequence: 1 tgccaggagaaacagaacac.....cacaagccacagagcctaga 584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 30108

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	3	16.6	2.8	26	13	BM399811	BM399811 5009-0-62
c	4	16.4	2.8	19	17	AZ788326	AZ788326 2M0035P16
	5	16.2	2.8	30	17	AZ464926	AZ464926 1M0274J04
	6	16.2	2.8	30	17	AZ875577	AZ875577 2M0190G06
c	7	16	2.7	25	9	AA936737	AA936737 oi59f10.s
	8	16	2.7	25	17	AZ348233	AZ348233 1M0084G04
	9	16	2.7	26	17	AZ823359	AZ823359 2M0097C19
	10	16	2.7	27	17	AZ343341	AZ343341 1M0076B04
	11	16	2.7	29	17	AZ474207	AZ474207 1M0290M03
	12	15.8	2.7	26	17	AZ994586	AZ994586 2M0280B08
c	13	15.8	2.7	27	17	AZ355810	AZ355810 1M0095G10
c	14	15.8	2.7	27	17	AZ842796	AZ842796 2M0141I20
	15	15.8	2.7	28	9	AI085431	AI085431 ow82h11.s
	16	15.8	2.7	28	9	AI635783	AI635783 wa07d11.x
	17	15.6	2.7	24	17	AZ435604	AZ435604 1M0222B13
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c	19	15.6	2.7	28	17	AZ609645	AZ609645 1M0434H02
	20	15.6	2.7	30	17	AZ320274	AZ320274 1M0040C18
	21	15.6	2.7	30	17	AZ323580	AZ323580 1M0045N05
	22	15.6	2.7	30	17	AZ389258	AZ389258 1M0149K12
c	23	15.6	2.7	30	17	AZ390605	AZ390605 1M0152P01
c	24	15.6	2.7	30	17	AZ412491	AZ412491 1M0186A03
	25	15.6	2.7	30	17	AZ465216	AZ465216 1M0275D04
	26	15.6	2.7	30	17	AZ468615	AZ468615 1M0281D22
	27	15.6	2.7	30	17	AZ487848	AZ487848 1M0317H13
c	28	15.6	2.7	30	17	AZ490365	AZ490365 1M0323J14
	29	15.6	2.7	30	17	AZ638210	AZ638210 1M0498C06
c	30	15.6	2.7	30	17	AZ764531	AZ764531 1M0560M15
	31	15.6	2.7	30	17	AZ788303	AZ788303 2M0035K15
	32	15.6	2.7	30	17	AZ807237	AZ807237 2M0069L19
	33	15.6	2.7	30	17	AZ824951	AZ824951 2M0099E19
c	34	15.6	2.7	30	17	AZ845409	AZ845409 2M0145N10
	35	15.6	2.7	30	17	AZ853274	AZ853274 2M0156D23
	36	15.6	2.7	30	17	AZ861881	AZ861881 2M0168J17
	37	15.6	2.7	30	17	AZ942781	AZ942781 2M0203P06
	38	15.4	2.6	25	9	AI762378	AI762378 wi54f10.x
c	39	15.4	2.6	27	17	AZ330939	AZ330939 1M0056E11
c	40	15.4	2.6	27	17	AZ495213	AZ495213 1M0331A04
c	41	15.4	2.6	30	17	AZ833458	AZ833458 2M0115L02
	42	15.2	2.6	23	17	AZ820760	AZ820760 2M0093K07
	43	15.2	2.6	28	17	AZ483923	AZ483923 1M0309A22
c	44	15.2	2.6	28	17	AZ947343	AZ947343 2M0210G06
c	45	15.2	2.6	29	17	AZ641783	AZ641783 1M0504E06

ALIGNMENTS

RESULT 1
AZ776616
LOCUS AZ776616 28 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0010K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0010K24 F, DNA sequence.
ACCESSION AZ776616
VERSION AZ776616.1 GI:12904394
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0010 row: K column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES Location/Qualifiers
source 1. .28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0010K24"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 12 c 3 g 6 t
ORIGIN

Query Match 2.9%; Score 16.8; DB 17; Length 28;
Best Local Similarity 75.0%; Pred. No. 6.9e+06;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy    491 CTGACCCCATCCTTGCGACAGCCCTCGC 518
          |||||| |||| |  ||| ||||| | |
Db      1 CTGACCTCATCATCTCGAAAGCCCACTC 28
```

RESULT 2
TA42E02P/c
LOCUS TA42E02P 30 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 42e02, forward sequence, genomic survey sequence.
ACCESSION AL455550
VERSION AL455550.1 GI:11856678
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 30)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .30
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="42e02"

BASE COUNT 7 a 11 c 6 g 6 t
ORIGIN

Query Match 2.9%; Score 16.8; DB 17; Length 30;
Best Local Similarity 75.0%; Pred. No. 6.9e+06;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy     59 ACGAGTGTGTCTCCTGTAGTAACTGTAA 86
          | ||||||||  ||||| | || ||| |
Db     29 AAGAGTGTGTGCCCTGTGGGAAGTGTCA 2
```

RESULT 3
BM399811/c
LOCUS BM399811 26 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-62-A04.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM399811
VERSION BM399811.1 GI:18199864
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 26)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES Location/Qualifiers
source 1. .26
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 7 a 7 c 8 g 4 t
ORIGIN

Query Match 2.8%; Score 16.6; DB 13; Length 26;
Best Local Similarity 82.6%; Pred. No. 7.6e+06;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    237 CCAACGGTGGAAGTCCAAGCTCT 259
          ||| |||||||  |||||||| |
Db     26 CCACCGGTGGAGCTCCAAGCTTT 4
```

RESULT 4
AZ788326/c
LOCUS AZ788326 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0035P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035P16 F, DNA sequence.

ACCESSION AZ788326
VERSION AZ788326.1 GI:12928014
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: P column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0035P16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 3 g 3 t
ORIGIN

Query Match 2.8%; Score 16.4; DB 17; Length 19;
Best Local Similarity 94.4%; Pred. No. 8.3e+06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 261 CTCCATTGTTTGTGGGAA 278
||||||||||.|||||||
Db 19 CTCCATTGTTGGTGGGAA 2

RESULT 5
AZ464926
LOCUS AZ464926 30 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0274J04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0274J04 R, DNA sequence.

ACCESSION AZ464926
VERSION AZ464926.1 GI:10623051
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0274 row: J column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.

FEATURES Location/Qualifiers
source 1. .30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0274J04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 29 c 0 g 0 t
ORIGIN

Query Match 2.8%; Score 16.2; DB 17; Length 30;
Best Local Similarity 72.4%; Pred. No. 9.7e+06;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 513 CCTCGCCTCCGACCCCATCCCCAACCCCC 541
|| | || || ||||| |||| |||||
Db 1 CCCCCCCCCCCCCCCCACCCCCCCCCCCC 29

RESULT 6
AZ875577
LOCUS AZ875577 30 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0190G06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0190G06 F, DNA sequence.

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ACCESSION   AZ875577
VERSION     AZ875577.1  GI:13085557
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0190  row: G  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0190G06"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a     28 c      1 g      1 t
ORIGIN

  Query Match             2.8%;  Score 16.2;  DB 17;  Length 30;
  Best Local Similarity   72.4%;  Pred. No. 9.7e+06;
  Matches   21;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    512 CCCTCGCCTCCGACCCCATCCCCAACCCC 540
          ||||| || ||  ||||  ||||  ||||
Db      1 CCCTCCCCCCCCCCCCCCCCCCCCCCCC 29


RESULT 7
AA936737/c
LOCUS       AA936737                 25 bp    mRNA    linear   EST 29-APR-1998
DEFINITION  oi59f10.s1 NCI_CGAP_HN4 Homo sapiens cDNA clone IMAGE:1486987 3'
            similar to TR:Q18444 Q18444 COSMID C34D4. ;, mRNA sequence.
ACCESSION   AA936737
VERSION     AA936737.1  GI:3094771
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Dental Research,
            Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: John Ensley, M.D.
            cDNA Library Preparation: Stratagene, Inc.
            cDNA Library Arrayed by: Greg Lenhon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1486987"
                     /clone_lib="NCI_CGAP_HN4"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: pharynx; Vector: Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. Average insert size 1.5 kb. 5' adaptor sequence:
                     5' GAATTCGGCACGAG 3' 3' adaptor sequence: 5' (GA
                     )10ACTAGTCTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT        1 a      1 c     18 g      5 t
ORIGIN

  Query Match             2.7%;  Score 16;  DB 9;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 1.1e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    521 CCGACCCCATCCCCAACCCCCTTC 544
          || |||||| ||| ||| |||| |
Db     25 CCCACCCCACCCCGAACACCCTCC 2


RESULT 8
AZ348233
LOCUS       AZ348233                 25 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0084G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0084G04 R, DNA sequence.
ACCESSION   AZ348233
VERSION     AZ348233.1  GI:10427470
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0084 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.

FEATURES Location/Qualifiers
source 1. .25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0084G04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 23 c 0 g 0 t
ORIGIN

Query Match 2.7%; Score 16; DB 17; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.1e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy     518 CCTCCGACCCCATCCCCAACCCCC 541
           || ||  ||||| ||||| |||||
Db       2 CCCCCCCCCCCACCCCCACCCCCC 25
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RESULT 9
AZ823359
LOCUS AZ823359 26 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0097C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0097C19 F, DNA sequence.
ACCESSION AZ823359
VERSION AZ823359.1 GI:12993267
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0097 row: C column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES Location/Qualifiers
source 1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0097C19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 9 g 3 t
ORIGIN

Query Match 2.7%; Score 16; DB 17; Length 26;
Best Local Similarity 79.2%; Pred. No. 1.1e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy     536 ACCCCCTTCAGAAGTGGGAGGACA 559
           ||||| ||||| ||||||   |||
Db       3 ACCCCATTCAGGAGTGGGGCCACA 26
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RESULT 10
AZ343341
LOCUS AZ343341 27 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0076B04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0076B04 R, DNA sequence.
ACCESSION AZ343341
VERSION AZ343341.1 GI:10421314
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

```
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076  row: B  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0076B04"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        5 a      7 c      8 g      7 t
ORIGIN

  Query Match             2.7%;  Score 16;  DB 17;  Length 27;
  Best Local Similarity   79.2%;  Pred. No. 1.1e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy     254 AGCTCTACTCCATTGTTTGTGGGA 277
           | | || |||||||| | ||||||
Db       3 AACACTCCTCCATTGCTGGTGGGA 26


RESULT 11
AZ474207
LOCUS       AZ474207                 29 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0290M03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0290M03 R, DNA sequence.
ACCESSION   AZ474207
VERSION     AZ474207.1  GI:10632332
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0290  row: M  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0290M03"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        5 a     11 c      4 g      9 t
ORIGIN

  Query Match             2.7%;  Score 16;  DB 17;  Length 29;
  Best Local Similarity   79.2%;  Pred. No. 1.1e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy     389 CCGTGCCCAGTTCCACCTTCACCT 412
           || ||||  | || ||||||||||
Db       5 CCTTGCCTGGATCTACCTTCACCT 28


RESULT 12
AZ994586
LOCUS       AZ994586                 26 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0280B08F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0280B08 F, DNA sequence.
ACCESSION   AZ994586
VERSION     AZ994586.1  GI:13865813
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0280 row: B column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES Location/Qualifiers
source 1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0280B08"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 13 c 0 g 4 t
ORIGIN

Query Match 2.7%; Score 15.8; DB 17; Length 26;
Best Local Similarity 89.5%; Pred. No. 1.2e+07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    414 CAGCTCCACCTATACCCCC 432
          || ||||||||||| |||
Db      1 CAACTCCACCTATACACCC 19
```

RESULT 13
AZ355810/c
LOCUS AZ355810 27 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0095G10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0095G10 R, DNA sequence.
ACCESSION AZ355810
VERSION AZ355810.1 GI:10468500
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: G column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES Location/Qualifiers
source 1. .27
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0095G10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 24 g 3 t
ORIGIN

Query Match 2.7%; Score 15.8; DB 17; Length 27;
Best Local Similarity 74.1%; Pred. No. 1.2e+07;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy    513 CCTCGCCTCCGACCCCATCCCCAACCC 539
          || | || || |||||  ||||| |||
Db     27 CCACCCCCCCCACCCCCCCCCCACCCC 1
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RESULT 14
AZ842796/c
LOCUS AZ842796 27 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0141I20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0141I20 F, DNA sequence.
ACCESSION AZ842796
VERSION AZ842796.1 GI:13012704
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

```
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0141  row: I  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0141I20"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        1 a      0 c     17 g      9 t
ORIGIN

  Query Match             2.7%;  Score 15.8;  DB 17;  Length 27;
  Best Local Similarity   74.1%;  Pred. No. 1.2e+07;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     396 CAGTTCCACCTTCACCTCCAGCTCCAC 422
           ||   ||||| ||||| ||| | ||||
Db      27 CACCACCACCATCACCACCACCACCAC 1


RESULT 15
AI085431
LOCUS       AI085431                 28 bp    mRNA    linear   EST 28-AUG-1998
DEFINITION  ow82h11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1653381 3' similar to TR:Q15409 Q15409 RTVP-1 PROTEIN.
            ;, mRNA sequence.
ACCESSION   AI085431
VERSION     AI085431.1  GI:3423854
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index.
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1938   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1653381"
                      /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                      /sex="male"
                      /dev_stage="20 week-post conception fetus"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                      with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                      This is a subtracted version of the original Soares fetal
                      liver spleen 1NFLS library.   1st strand cDNA was primed
                      with a Pac I - oligo(dT) primer [5'
                      AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Pac I and cloned into the Pac I
                      and Eco RI sites of the modified pT7T3 vector.  Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT        8 a      4 c     10 g      6 t
ORIGIN

  Query Match             2.7%;  Score 15.8;  DB 9;  Length 28;
  Best Local Similarity   74.1%;  Pred. No. 1.2e+07;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      76 AGTAACTGTAAGAAAAGCCTGGAGTGC 102
           || |||| || |  ||| ||||||||
Db       2 AGAAACTTTAGGGCAAGGTTGGAGTGC 28


Search completed: May 21, 2003, 07:30:04
Job time : 1444 secs
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